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Figure 1A

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121 tgatcctacgaaaaagaggtaaatggatactggcggcaattcgctggcgtccggacctgat  
M D T G G N S L A S G P D 133  
181 ggtgtgaagaggaaagtgtttatatttctatgacctgaggtcggaattactactatggc  
G V K R K V C Y F Y D P E V G N Y Y Y G 333  
241 caaggtcatccatgaagccccatcgcatccgatgacctgacctccctccgctccactac  
Q G H P M K P H R I R M T H A L L A H Y 533  
301 ggtctccttcagcatatgcaggttctcaagcccttccctgcccgcgaacgtgactctctgc  
G L L Q H M Q V L K P F P A R E R D L C 733  
361 cgttccacgcgcgacgactatgctctcttttctcccgacgattacccctgaaacccagcaa  
R F H A D D Y V S F L R S I T P E T Q Q 933  
421 gatcagattcgccaacttaagcgttctcaatggttgatgaagactgtcccgctctttgacggc  
D Q I R Q L K R F N V G E D C P V F D G 1133  
481 ctttattccttttgccagacctatgctggaggatctgttggtggctctgtcaagcttaac  
L Y S F C Q T Y A G G S V G G S V K L N 1333  
541 cagggcctctgcgatattgccatcaactgggctgggtggtctccatcacgctaagaagtgc  
H G L C D I A I N W A G G L H H A K K C 1533  
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E A S G F C Y V N D I V L A I L E L L K 1733  
661 cagcatgagcgtgtttctttatgtcgatattgatatccaccacggggatggagtgaggag  
Q H E R V L Y V D I D I H H G D G V E E 1933  
721 gcattttatgctactgacaggggtatgactgtctcgtttcataaatttggltgattacttt  
A F Y A T D R V M T V S F H K F G D Y F 2133  
781 cccggtacaggtcacattcaggatataggttatggttagcggaaagtactattctctcaat  
P G T G H I Q D I G Y G S G K Y Y S L N 2333  
841 glaccactggatgatggaatcgatgatgagagctatcatctgttattcaagcccatcatg  
V P L D D G I D D E S Y H L L F K P I M 2533  
901 gggaaagtattggaattttccgaccaggggctgtgggtattgcaatgtgggtgctgactcc  
G K V M E I F R P G A V V L Q C G A D S 2733  
961 ctatctggggatcggttaggttgcttcaatctttcaatcaaaggtcatgctgagtgcgtc  
L S G D R L G C F N L S I K G H A E C V 2933  
1021 aaatttatgagatcggttcaatggttccctactgctcttgggtgggtgggtggttacctatc  
K F M R S F N R V P L L L G G G G Y T I 3133  
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E A V E P D T K D K D G L K G I M E R G 4533  
1501 aaaggttgtgaggtggaggtggatgagagtggaagcactaaaggttacaggagtaaaccca  
K G C E V E V D E S G S T K V T G V N P 4733  
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V G V E E A S V K M E E E G T N K G G A 4933  
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E Q A F P K T + 501  
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1801 atgaaaa



Figure 1B

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61 taaaacttggaatagagagagactctgagtgaagagagattctgagtgaagacggag  
121 atggaggcagacgaaagcggcatctctctgccgtcgggacccgacggacgtaagcggcga  
M E A D E S G I S L P S G P D G R K R R 20  
181 gtcagttacttctacgagcgcgacgatcggagactactactacgggtcaagccaccgatg  
V S Y F Y E P T I G D Y Y Y G Q G H P M 40  
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E Y V D F L A S V S P E S M G D P S A A 100  
421 cgaaacctaaaggcgattcaatgtcgggtgaggattgtcctgtcttcgacggactttttgat  
R N L R R F N V G E D C P V F D G L F D 120  
481 ttttgccgtgcttccgcccggaggttctattgggtgctgcccgtcaaattaaacagacaggac  
F C R A S A G G S I G A A V K L N R Q D 140  
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A D I A I N W G G G L H H A K K S E A S 160  
601 gggttttgctatgtaaacgacatcgtgctagggattctggagttgctcaagatgtttaag  
G F C Y V N D I V L G I L E L L K M F K 180  
661 cgggttctctacatagatattgatgtccaccatggagatggagtggagaagcgtttttac  
R V L Y I D I D V H H G D G V E E A F Y 200  
721 accactgatagagttatgactgtttctttccacaaatttggggactttttccagggaact  
T T D R V M T V S F H K F G D F F P G T 220  
781 ggtcacataagagatgttggcgtgaaaaagggaaatactatgctctaaatgttccacta  
G H I R D V G A E K G K Y Y A L N V P L 240  
841 aacgatggatggacgatgaaagtttccgcagcttgttttagacctcttatccagaagggt  
N D G M D D E S F R S L F R P L I Q K V 260  
901 atggaagtgtatcagccagaggcagttgttcttcagtgtggtgctgactccttaagtgg  
M E V Y Q P E A V V L Q C G A D S L S G 280  
961 gatcgggttgggttgccttcaacttatcagtcgaagggtcacgctgattgccttcgggttctta  
D R L G C F N L S V K G H A D C L R F L 300  
1021 agatcttacaacgttccctctcatggtgttgggtgggtgaagggtatactattcgaaatgtt  
R S Y N V P L M V L G G E G Y T I R N V 320  
1081 gcccggttgcgtgttatgagactgcagttgctgttggagtagagccggacaacaaactc  
A R C W C Y E T A V A V G V E P D N K L 340  
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P Y N E Y F E Y F G P D Y T L H V D P S 360  
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P M E N L N T P K D M E R I R N T L L E 380  
1261 caacttttcgggactaatacacgcacctagcgtccagtttcagcacacaccaccagtcatt  
Q L S G L I H A P S V Q F Q H T P P V N 400  
1321 cgagtttttgacgagccggaagatgacatggagacaagacccaaaacctcgcatctggagt  
R V L D E P E D D M E T R P K P R I W S 420  
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G T A T Y E S D S D D D D K P L H G Y S 440  
1441 tgtcgtggtggcgcaactacggacagggactctaccggtgaagatgaaatggatgacgat  
C R G G A T T D R D S T T G E D E M D D 460  
1501 aaccagagccagacgtgaatcctccatcgtcttaaaaccagcttgatgggttgggtgtctc  
N P E P D V N P P S S \* 471  
1561 ttttgccatatgataatgtcggcagatttaagaaacaagttagggggaatgaatgattctt  
1621 tgatgttttttcagcaaccttttgatgtctgtgaaaaacgttgcattgattagaacagtga  
1681 caactgactagtatttttgcccaagttagaanaatcagaatatgtgaaaaaaaaaaaaaa  
1741 aaaaaaaaggcggcgcgtctagaggatccaagcttacgtacgcgtgcacgtcat

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## Figure 2A

1 cacgcgtccgtaaaaatcctctcttttttctcaaccttgattcttagccatggagttcttgg  
M E F W 4  
61 ggaattgaagttaaatcaggaaagccagttacagtgactcctgaagaaggcattcttatac  
G I E V K S G K P V T V T P E E G I L I 24  
121 cacgtttctcaggcatcgtttggagaatgtaaaaacaagaaggagagtttgtgccttta  
H V S Q A S L G E C K N K K G E F V P L 44  
181 catgtaaaggttgggaaccagaacttggttctgggaactctatcgactgagaacatccct  
H V K V G N Q N L V L G T L S T E N I P 64  
241 cagcttttctgtgatttgggtatttcgacaaggagtttgagctttctcacacttggggaaaa  
Q L F C D L V F D K E F E L S H T W G K 84  
301 ggaagtgtttactttgttggatacaaaaactcccaacattgagccacaaggctattctgag  
G S V Y F V G Y K T P N I E P Q G Y S E 104  
361 gaagaagaggaagaagaggaagaagttcctgctgggaatgctgccaaaggctgtagctaaa  
E E E E E E E V P A G N A A K A V A K 124  
421 ccaaaggctaagcctgcagaagtgaagccagctgttgatgatgaagaggatgagctctgat  
P K A K P A E V K P A V D D E E D E S D 144  
481 tctgacggaatggatgaagatgattctgatggtgaggattctgaggaagaagagcctaca  
S D G M D E D D S D G E D S E E E E P T 164  
541 cctaagaagcctgcatcaagcaagaagagagctaataaaactaccctaaagcacctgtg  
P K K P A S S K K R A N E T T P K A P V 184  
601 tcagcaaagaaggcgaaagtagcagttactcctcagaaaaacagatgagaagaagaaaggg  
S A K K A K V A V T P Q K T D E K K K G 204  
661 ggaaaggctgcaaaccagagcccaaaagtcggccagtcaggtctcatgtggttcatgcaag  
G K A A N Q S P K S A S Q V S C G S C K 224  
721 aagactttcaactcaggggaatgcacttgagttctcacaacaaggccaagcacgctgctgcc  
K T F N S G N A L E S H N K A K H A A A 244  
781 aagtgaagtgggtttcttattagagcttgtgatttctatggaattttgcctgtagctcttta  
K \* 245  
841 tgaaaccttcggattttcttatattttcttttgataacaagagtcttaatgaaagagagc  
cagttggagtccttaaaaaaaaaaaaaaaaaagggcgccgc



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Figure 3

AtRPD3A	MD-----TGG	NSIAS--GPDG	VKRKVCYFYD	PEVGNYYYGQ	GHPMKPHRIR	44
AtRPD3B	MEADESGI--	-SLPS--GPDG	PKRRVSYFYE	PTIGDYYYGQ	GHPMKPHRIR	47
ZmRPD3	MDPSSAGSGG	NSLPSVGPDG	QKRKVCYFYD	PDVGNYYYGQ	GHPMKPHRIR	50
RPD3	MVYEATPFD-	---PITVKPS	DKRRVAYFYD	ADVGNYYAYGA	GHPMKPHRIR	46
AtRPD3A	MTHALLAHYG	LLQHMOVLPK	FPARERDLCR	FHADDYVSFL	RSITPETQQD	94
AtRPD3B	MAHSLIITHYH	LHRRLEISRP	SLADASDIGR	FHSPEYVDFL	ASVSPESMGD	97
ZmRPD3	MTHSLLARYG	LLNQMOVYRP	NPARERELCR	FHAEEYINFL	RSVTPETQQD	100
RPD3	MAHSLIMNYG	LYKKMEIYRA	KPATKQEMCQ	FHTDEYIDFL	SRVTPDNLEM	96
AtRPD3A	QI--RQLKRF	NVGEDCPVFD	GLYSFCQTYA	GGSVGGSVKL	NHGLCDIAIN	142
AtRPD3B	PSAARNLRRF	NVGEDCPVFD	GLFDFCRASA	GGSIGAAVKL	NRQDADIAIN	147
ZmRPD3	QI--RLKRF	NVGEECPVLD	GLYSFCQTYA	GASVGGAVKF	NHGH-DIAIN	147
RPD3	--FKRESVKF	NVGDDCPVFD	GLYEYCSISG	GGSMGAARL	NRGKCDVAVN	144
AtRPD3A	WAGGLHHAKK	CEASGFCYVN	DIVLAILELI	KQHERVLYVD	IDIHHDGDVE	192
AtRPD3B	WGGGLHHAKK	SEASGFCYVN	DIVLGILELI	KMKFRVLYID	IDVHHGDGVE	197
ZmRPD3	WSGGLHHAKK	CEASGFCYVN	DIVLAILELI	KHHERVLYVD	IDIHHDGDVE	197
RPD3	YAGGLHHAKK	SEASGFCYLN	DIVLGIIELI	RYHPRVLYID	IDVHHGDGVE	194
	**	*		* * **		
AtRPD3A	EAFYATDRVM	TVSFHKFGDY	FPGTGHIQDI	CYGSCKYYSL	NVPLDDGIDD	242
AtRPD3B	EAFYTDRVM	TVSFHKFGDF	FPGTGHIRDV	GAEKGKYAL	NVPLNDGMDD	247
ZmRPD3	EAFYTDRVM	TVSFHKFGDY	FPGTGDIRDI	GHSKGKYSL	NVPLDDGIDD	247
RPD3	EAFYTDRVM	TCSEHKYGEF	FPGTGELRDI	GVGAGKNYAV	NVPLRDGIDD	244
	*	* *				
AtRPD3A	ESYHL LFKPI	MCKVMEIFRP	GAVVLQCGAD	SLSGDRLGCF	NLSIKGHAEC	292
AtRPD3B	ESFRSLRPL	TQKVMFYQF	EAVVLQCGAD	SLSGDRLGCF	NLSVKGHADC	297
ZmRPD3	ESYQSLFKPI	MCKVMEVFRP	GAVVLQCGAD	SLSGDRLGCF	NLSIKGHAEC	297
RPD3	ATYRSVFEPV	IKKIMEWYQF	SAVVLQCGGD	SLSGDRLGCF	NLSMKGHANC	294
AtRPD3A	VKFMRSFNVP	LLLGGGGYGT	IRNVARCWCY	ETGVALGVEV	EDKMEHEYY	342
AtRPD3B	LRFLRSYNVP	LMVLGGEYGT	IRNVARCWCY	ETAVAVGVEP	DNKLPYNEYF	347
ZmRPD3	VRYMRSFNVP	LLLGGGGYGT	IRNVARCWCY	ETGVALGQEP	EDKMEVNEYF	347
RPD3	VNYVKSEGIP	MMVVGGGGYT	MRNVARTWCF	ETGLLNNVVL	DKDLPYNEYF	344
AtRPD3A	EYFGPDYTLH	VAPSNMENKN	SRQMLEEIRN	DLIHNLKLO	HAPSVPFQER	392
AtRPD3B	EYFGPDYTLH	VDPSNMENKN	TPKDMERIRN	TLLHNLGLI	HAPSVQFQHT	397
ZmRPD3	EYFGPDYTLH	VAPSNMENKN	TRQQIDDIRS	---KLSKLR	HAPSVHFQER	393
RPD3	EYYGPDYKLS	VRPSNMFNVN	TPEYLDKVMT	NI FANLENTK	YAPSVQLNHT	394
AtRPD3A	PPDTE TPEVD	EDQEDGDKRW	DPDSDMDVDD	D-----R	KPIPSRVKRE	434
AtRPD3B	PFVNRVLD--	-----	EPEDDME---	-----TR	KP---RIWSG	421
ZmRPD3	VPDTEIPEQD	EDQDDPDERH	DPDSDMEVDD	HKAVEESRR	SILGIIKIRE	443
RPD3	P-----	-----R-	DAEDLGDVEE	DSA-----	-----	409
AtRPD3A	AVEPD TKDKD	GLKGIMERGK	GCEVEVDESG	STKVT---GV	NPVGVBEAS-	480
AtRPD3B	TATYESDSD	DDKPL--HGY	SC-----	--RGGATTDR	DSTGEDEMDD	459
ZmRPD3	FGENATRVD	GGRVASEH-R	GLEPMAEDIG	SSKQAPQADA	SAMAI DEPSN	492
RPD3	-----	-----	-----	-----	-----EAKD	413
AtRPD3A	VKMEEBEGTNK	GGAEQAEPFK	T			501
AtRPD3B	DNPEFDVNP-	-----PSS				471
ZmRPD3	VKNEPESSTK	LOGQAAYHK	P			513
RPD3	TKGGSQYARD	LHVEHDNEFY				433

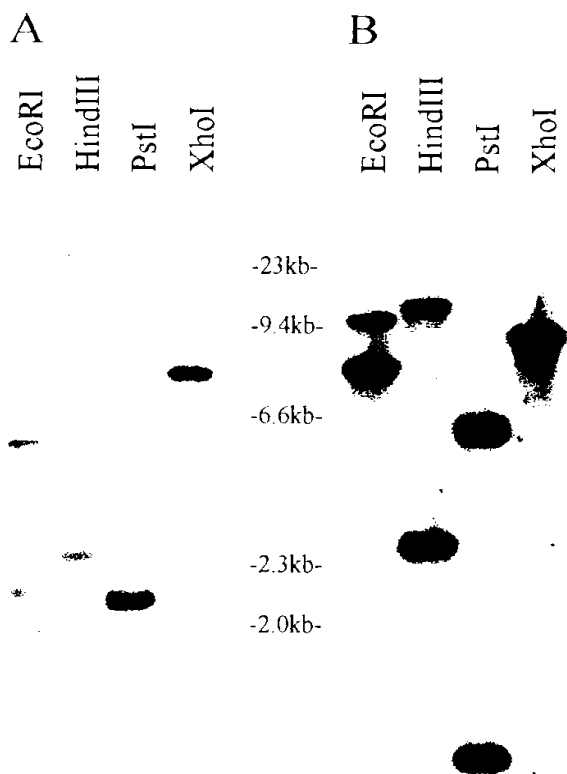


Figure 4

AtHD2A	MEFWCI	EVFS	SKPVT	VTPEE	GILIH	VSOAS	LGECKN	FKGE	FVPL	HVKVGN	50
AtHD2B	MEFWCV	ATTE	KNAT	VTPEE	DSL	VHISQAS	I-D	TVFSGE	SVVLS	VTVGG	49
ZmHD2	MEFWCL	EVFF	GSTV	CEFGY	GFVL	HLSQAA	LGES	--KPSD	NALMY	VKIDD	48
*											
AtHD2A	QNLV	LSTLST	ENIP	QLFCDI	VFDKE	FELSH	IWG	FGSVYEV	GYK	TPNIE	PQ 100
AtHD2B	AKLV	IGTISQ	DEFP	QISEDL	VFDKE	FELSH	SGTH	ANVHAI	GYE	SPNIE	QD 99
ZmHD2	QKIA	IGTISV	DENP	HIQFDL	IFDKE	FELSH	TSKTT	SVFET	GYE	VEQPFEE	98
*											
AtHD2A	GYSE	EEEE	E-	EEVP	PAGNAA	-----	---	KAVAKPK	AKPA	EVKPAV	136
AtHD2B	DFTSS	ODEEV	PEAV	PAPAPT	AVTANG	NAGA	AVV	KADTKPH	AKPA	EVKPAE	149
ZmHD2	DEMDDL	DEDE	DEEL	NVP--	VVKENG	KADE	KKQ	KSOEKAV	AA	PSKSSPDS	145
*											
AtHD2A	----	DDEEDE	SDS-	E-----	-----	GMD	EDDS	DGEDSE	EEE	-----	162
AtHD2B	EKPES	DEEDE	SDDE	CESEED	--	DDSEK	GMD	VDEDD	SDDD	EE	SEDEEEEE 197
ZmHD2	KKSKD	DDSD	EDET	ODSDED	ET	DDSD	DECLS	SEEG	DDSSD	ED	DTSDDEEE 195
-----											
AtHD2A	PTP--	KKLAS	-S	KKRAN	TT	PFAP	VSA	FA	KVAV	----TE	OKTDEK--- 202
AtHD2B	ETP--	KKPEP	IN	KKRP	NESV	SKTE	VSG	KKA	KPAA	AAPASTP	OK-----TEK 240
ZmHD2	DTPT	KKPEV	GK	RP	ESSV	LKTPL	DE	KKA	KVAT	PSS---	OKTGGK---- 238
-----											
AtHD2A	-KGG	KA----	-----	-----	-----	AN	QSPK	SASQVS	CGSC	-KFTFN	229
AtHD2B	KKGG	--HTAT	PHPA	F-----	KGGS	SPVNAN	QSPK	SGGQSS	GNNN	KKPEN	283
ZmHD2	-KGA	AVHVAT	PHPA	KGTIV	NNDK	SVKSPK	SAPK	SGGSVP	CKP	CSK-SFI	286
-----											
AtHD2A	SGNALE	-SHN	KAK	HAAAK							245
AtHD2B	SGKQ	FGGSNN	SGSN	KGKGK	RA						305
ZmHD2	SETAL	QA-HS	RA	MGASESQ	VQ						307



FIGURE 5









**FIGURE 7**

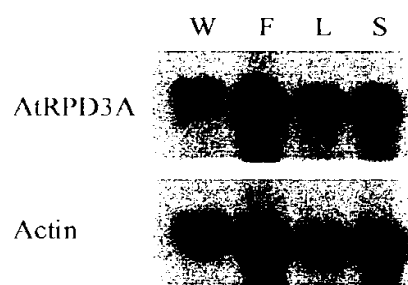
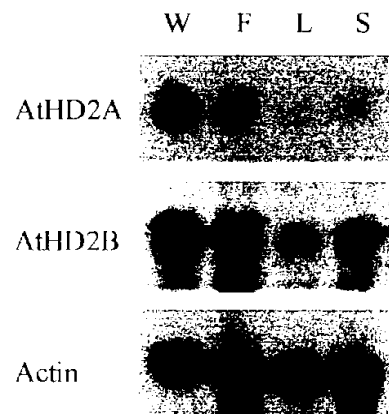




FIGURE 8





**Figure 9**

**A**

**Effector Plasmids**

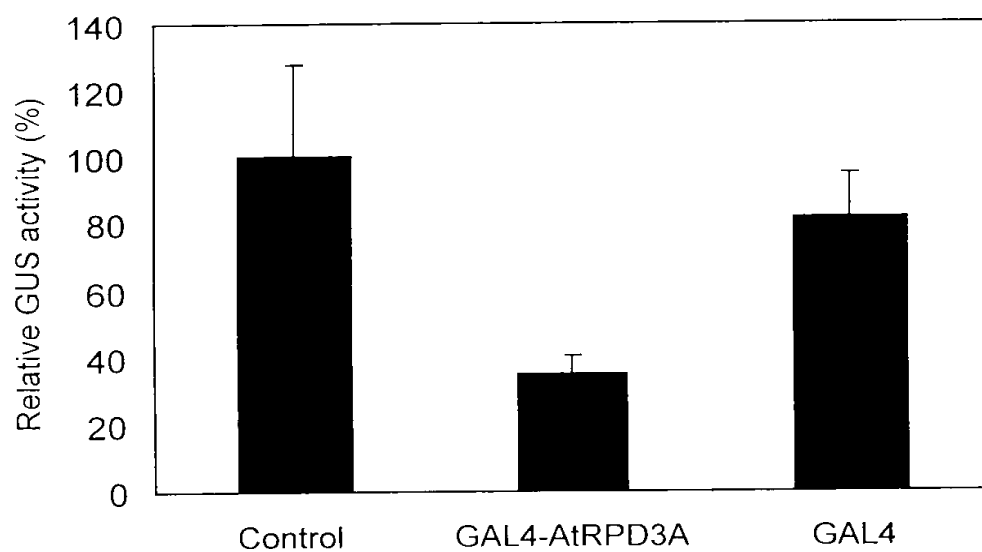
**GAL4-AtRPD3A** — [tCUP] — [GAL4BD] — [AtRPD3A] — [Nos-T]

**GAL4** — [tCUP] — [GAL4BD] — [Nos-T]

**Reporter Plasmid**

**UAS<sub>GAL4</sub>-tCUP-GUS** — [UAS<sub>GAL4</sub>] — [-394-tCUP] — [GUS] — [Nos-T]

**B**

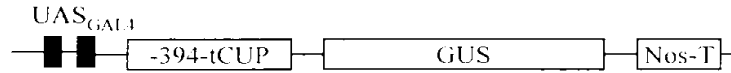


### Figure 10

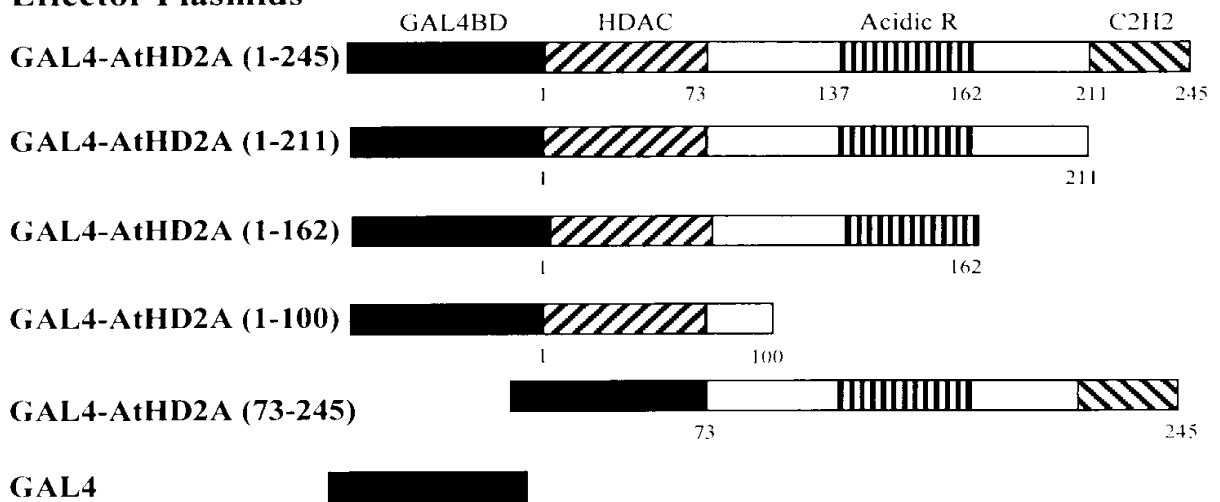
A

## Reporter Plasmid

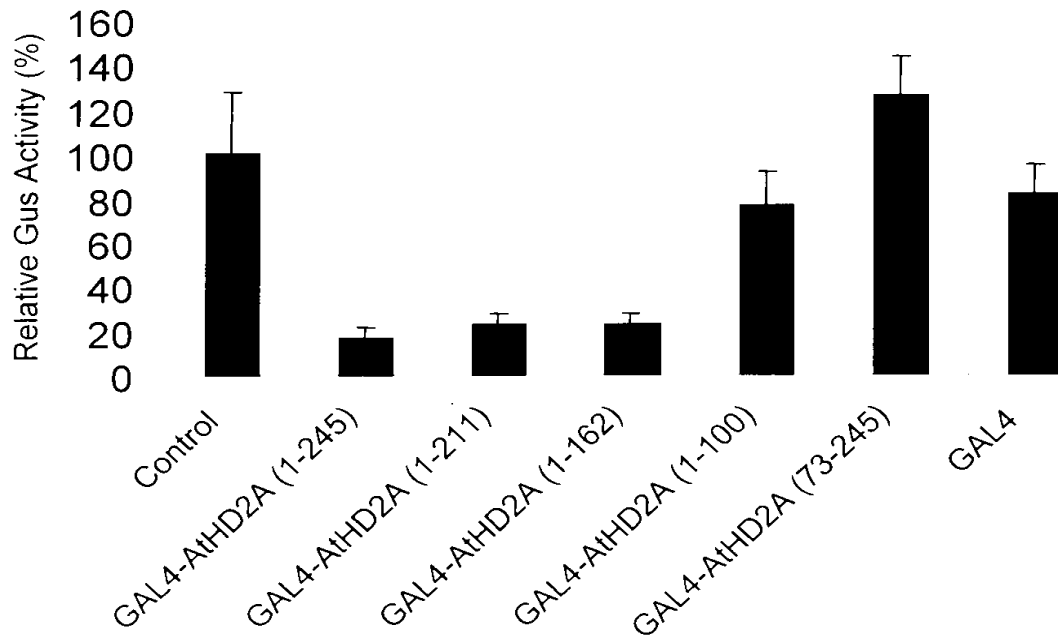
**UAS<sub>GAL4</sub>-tCUP-GUS**



## Effector Plasmids



B

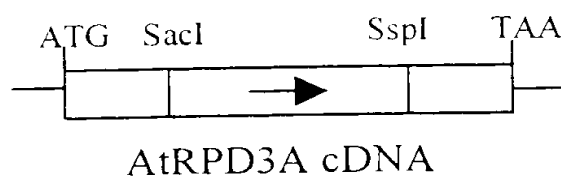




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## FIGURE 11

**A**



**B**

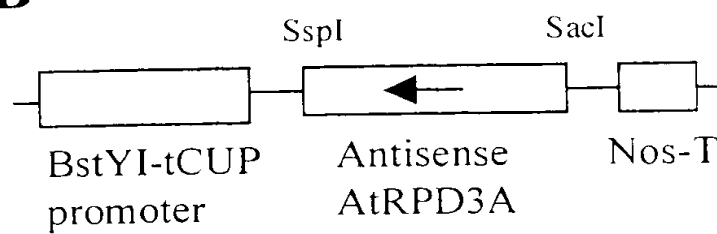




FIGURE 12

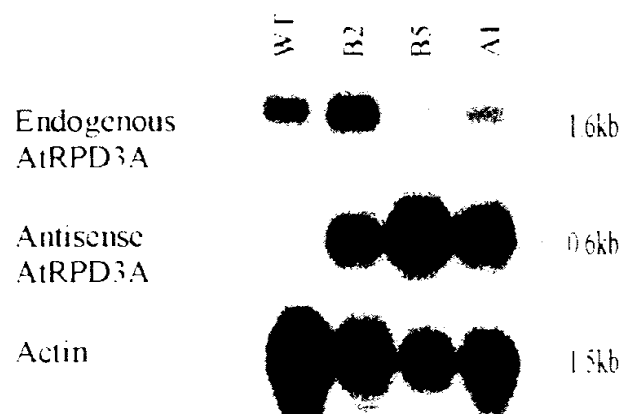




FIGURE 13

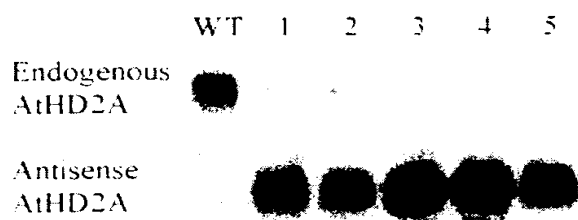
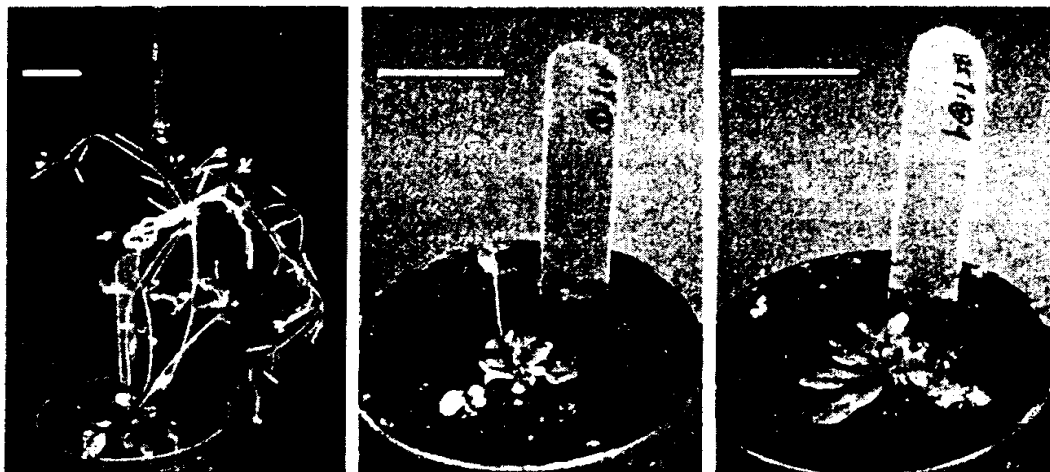


FIGURE 14







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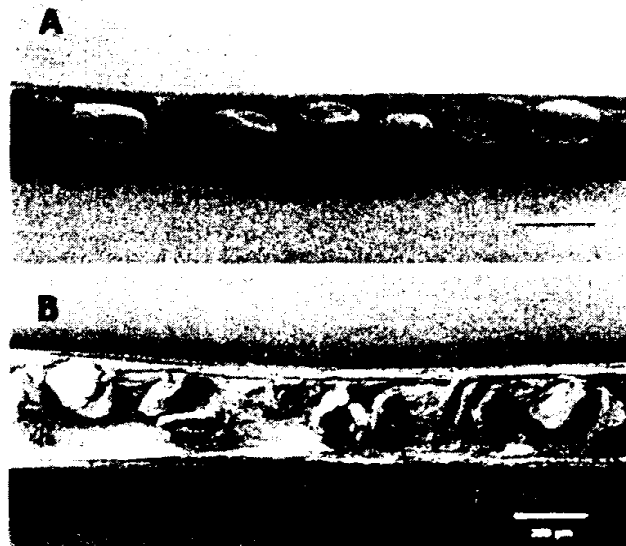
TECH CENTER 1600/2900

FIGURE 15



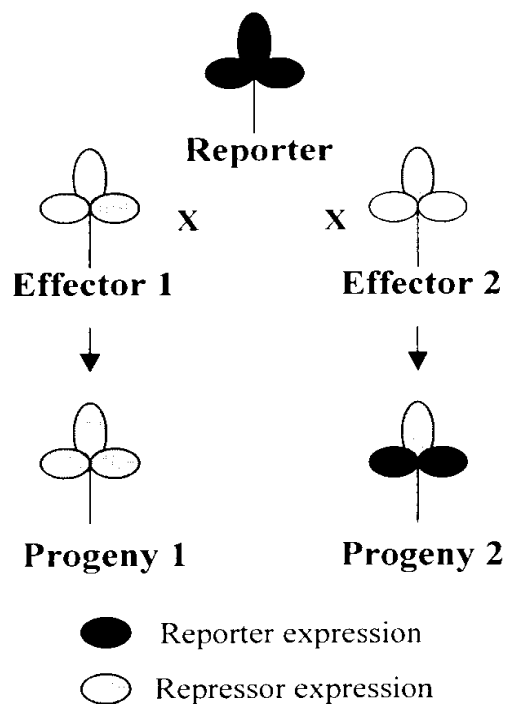


FIGURE 16





**A**



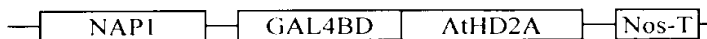
**B**

### Effector Plasmids

tCUP-GAL4/AtHD2A (Effector 1)

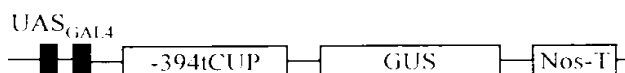


NAP1-GAL4/AtHD2A (Effector 2)

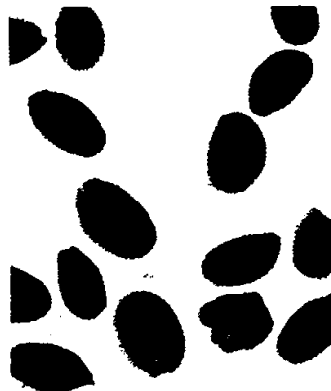
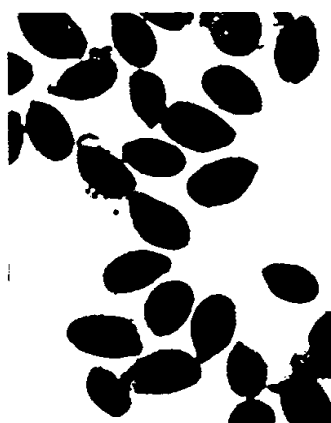


### Reporter Plasmid

UAS<sub>GAL4</sub>-tCUP-GUS (or UAS<sub>GAL4</sub>-35S-GUS)



**Figure 17**



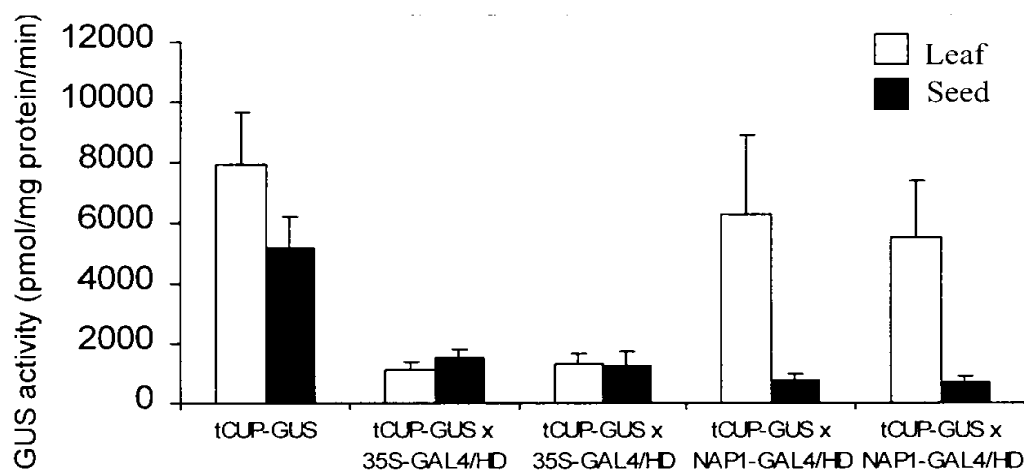


Figure 19A

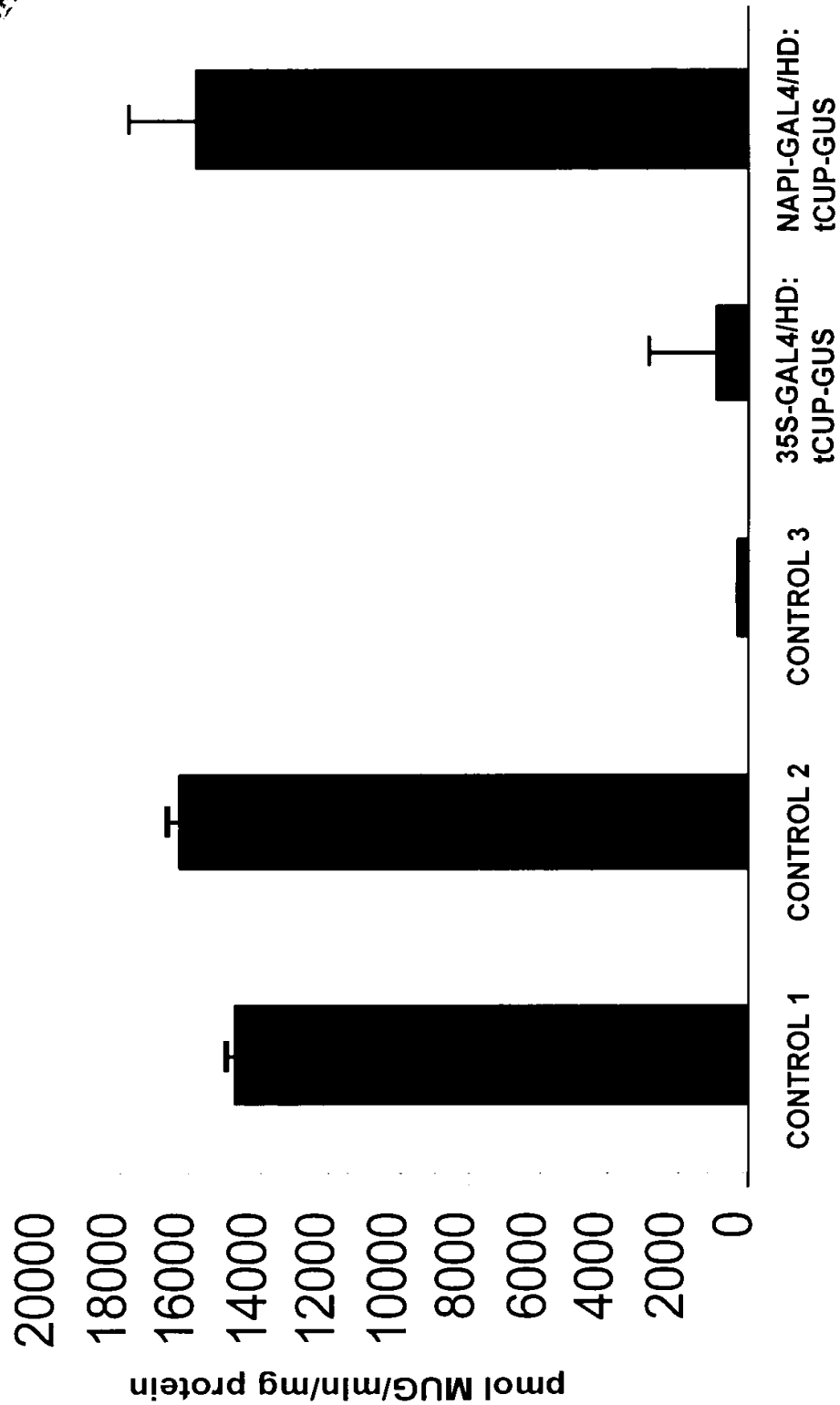


Figure 19B

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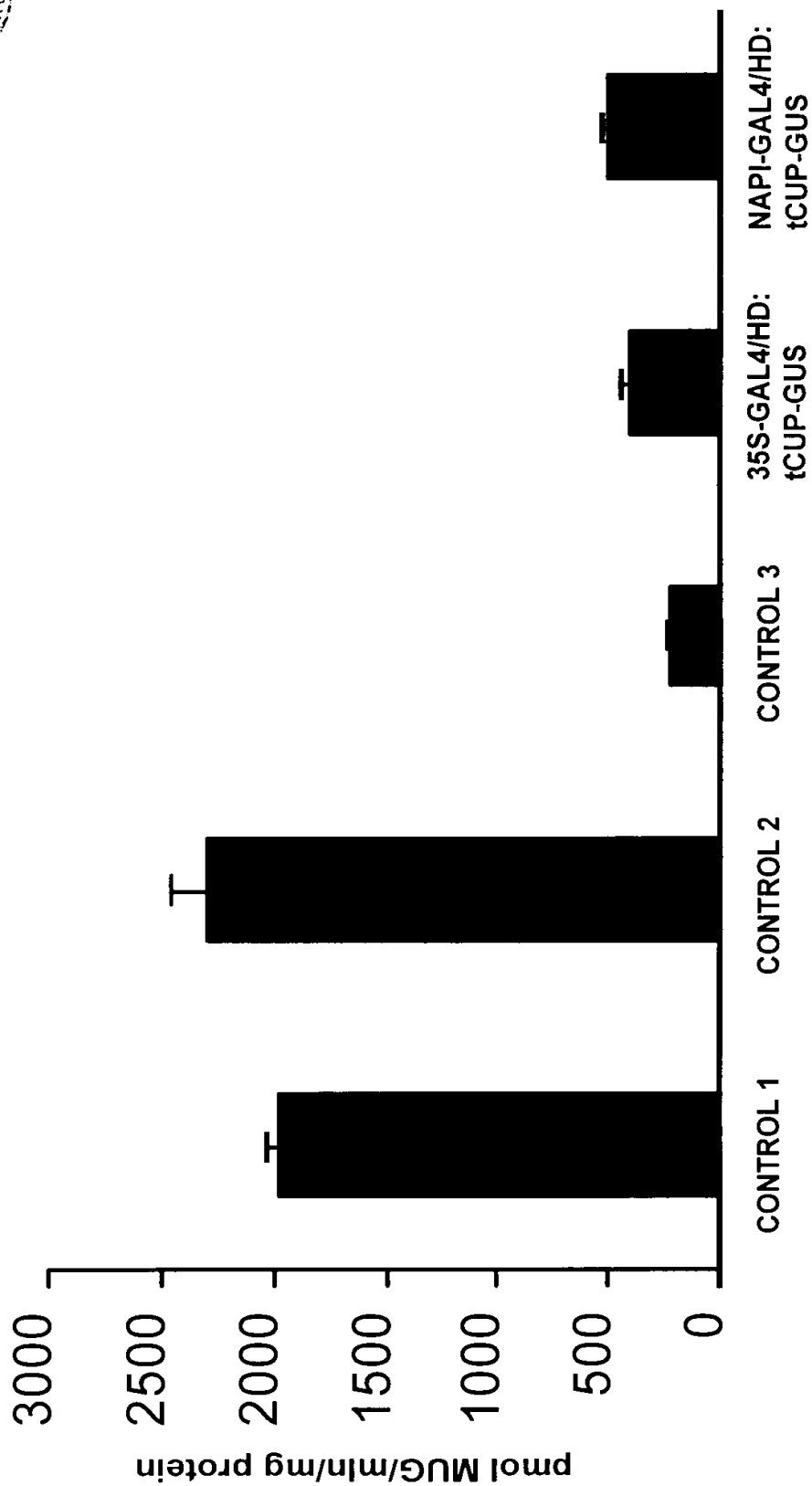
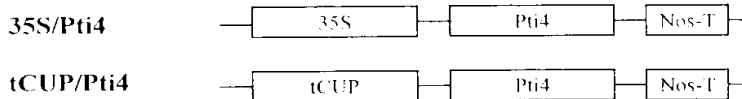


Figure 19C

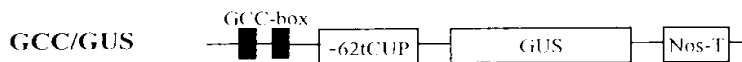


**A**

**Effector Plasmids**



**Reporter Plasmid**



**B**

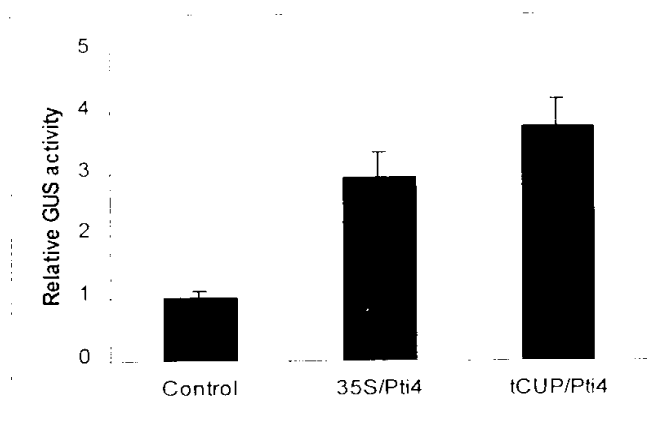


Figure 20



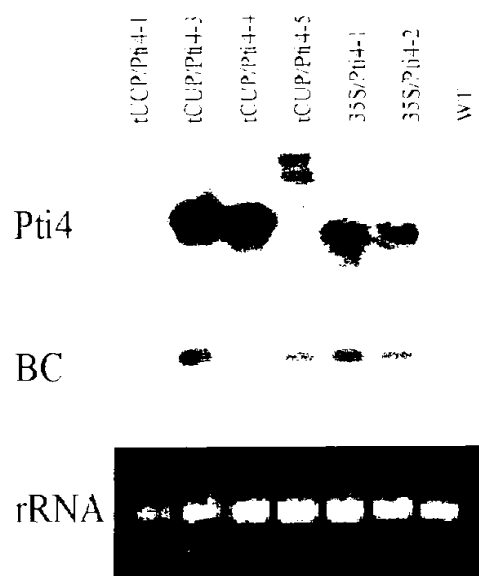


Figure 21

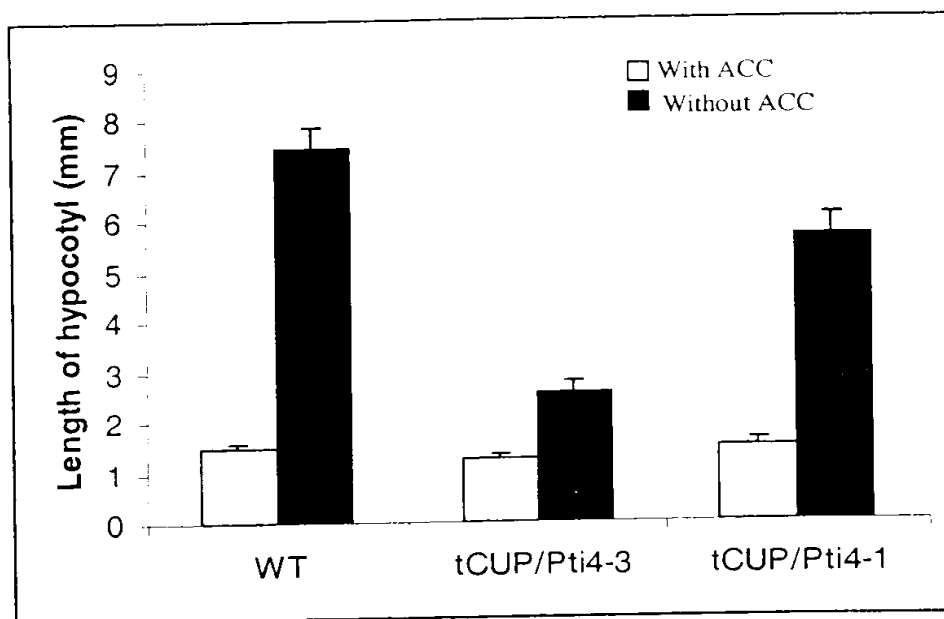


Figure 22

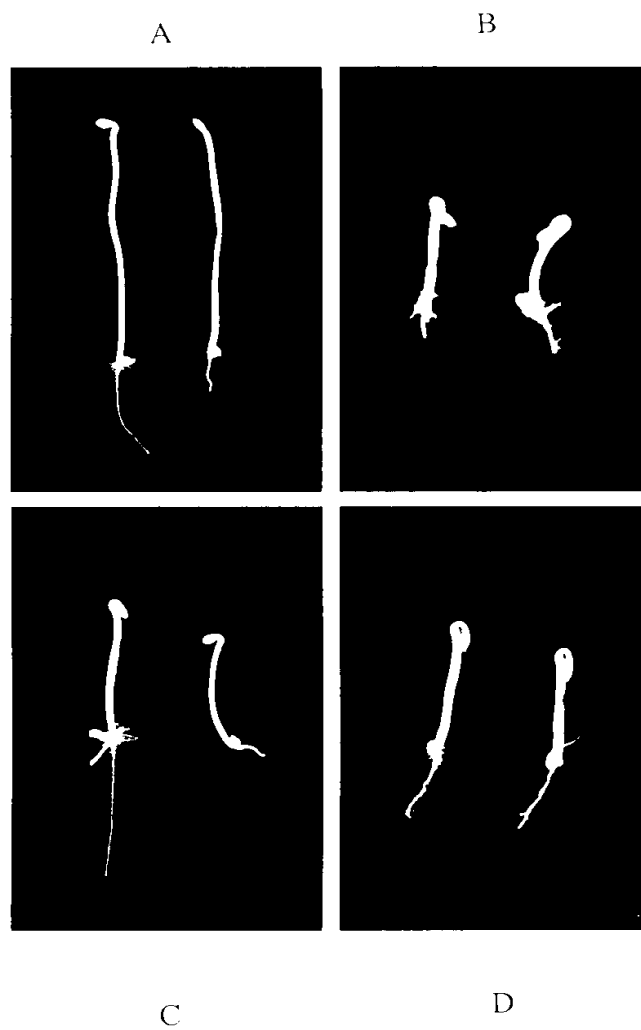


Figure 23

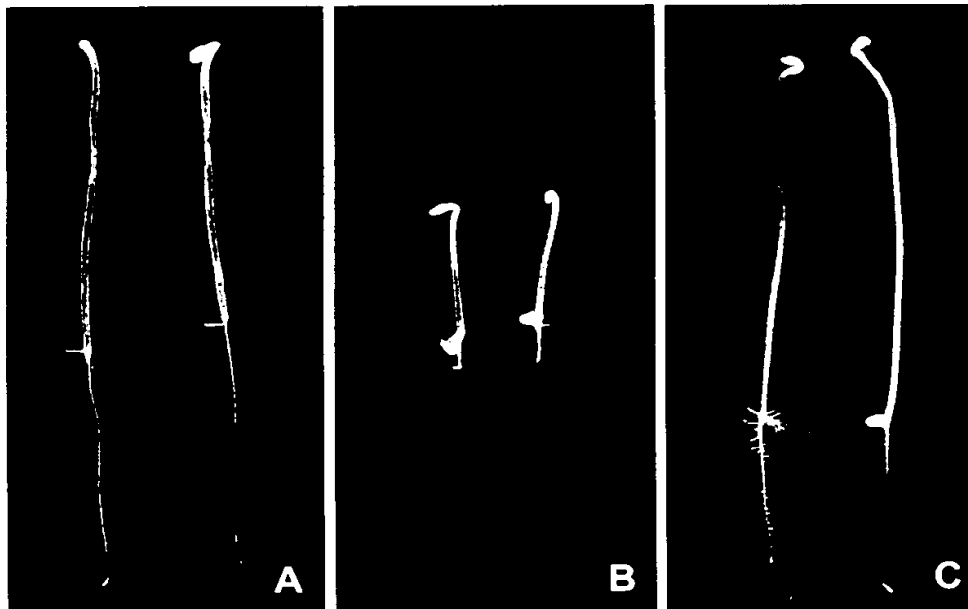


Figure 24